 IMPORTANCE OF NOVEL SEQUENCE ALTERATIONS IN THE FHIT GENE ON FORMATION OF BREAST CANCER

Gülsah Çeçener¹, Ünal Egeli¹, Berrin Tunca¹, İsmet Taşdelen², Şahsine Tolunay³, and Nazan Bilgel⁴

¹Department of Medical Biology, ²Department of Surgery, ³Department of Pathology, ⁴Department of Family Medicine, Faculty of Medicine, Uludag University, Bursa, Turkey

Aims and background: The character, role and impact of FHIT gene alterations, for which recent studies have shown that the gene has a role in the early stage of carcinogenesis in breast cancer, are still unclear. Thus, the current study evaluated FHIT gene mutations from breast tissue of women with malignant and benign breast disease and to elucidate the frequency and type of mutations in this gene.

Patients and methods: Mutations in exons 5-9 of the FHIT gene were screened using the intronic primer pairs in 83 breast (67 malignant and 16 benign) tissue samples by single-strand conformational polymorphism and sequencing analysis.

Key words: benign breast diseases, exonic splicing enhancers, FHIT gene, malignant breast disease, novel mutations, single-strand conformational polymorphism.

Results: FHIT mutations were detected in 13 of the 67 malignant cases (19.4%) and 2 of the 16 benign cases (12.5%). Four different sequence variants were determined: two novel frame shift mutations (codon 90 insA, codon 146 delT), one intronic novel mutation (IVS8 -17 insA), and one previously identified silent transition type alteration (codon 88 C to T). In addition, determination of this silent alteration caused formation of new exonic splicing enhancer (ESE) motifs on mutated sequences by using the ESEfinder program.

Conclusions: Our data contribute significantly to that currently known about the presence of FHIT gene mutations on the formation of breast cancer.